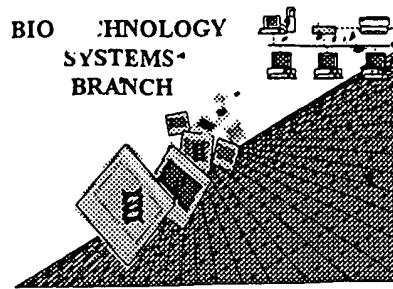


RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/015078

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THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

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FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).

Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
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OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/015,078

DATE: 09/10/2001
TIME: 09:39:29

Input Set : A:\235673-1.app
Output Set: N:\CRF3\09102001\I015078.raw

Does Not Comply
Corrected Diskette Needed

SEQUENCE LISTING

4 (1) GENERAL INFORMATION:

6 (i) APPLICANT: Suerbaum, Sebastian
7 Labigne, Agnes

9 (ii) TITLE OF INVENTION: Cloning and Characterization of the *flbA*
10 Gene of *H. Pylori*, Production of Aflagellate Strains

12 (iii) NUMBER OF SEQUENCES: 13

14 (iv) CORRESPONDENCE ADDRESS:

15 (A) ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
16 Dunner

17 (B) STREET: 1300 I Street, N.W.

18 (C) CITY: Washington

19 (D) STATE: D.C.

20 (E) COUNTRY: USA

21 (F) ZIP: 20005-3315

23 (v) COMPUTER READABLE FORM:

24 (A) MEDIUM TYPE: Floppy disk

25 (B) COMPUTER: IBM PC compatible

26 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

27 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

29 (vi) CURRENT APPLICATION DATA:

30 (A) APPLICATION NUMBER: US/09/015,078

C--> 31 (B) FILING DATE: 23-Aug-2001

32 (C) CLASSIFICATION:

34 (viii) ATTORNEY/AGENT INFORMATION:

35 (A) NAME: Meyers, Kenneth J.

36 (B) REGISTRATION NUMBER: 25,146

37 (C) REFERENCE/DOCKET NUMBER: 02356.0073-01000

39 (ix) TELECOMMUNICATION INFORMATION:

40 (A) TELEPHONE: (202) 408-4000

41 (B) TELEFAX: (202) 408-4400

44 (2) INFORMATION FOR SEQ ID NO: 1:

46 (i) SEQUENCE CHARACTERISTICS:

47 (A) LENGTH: 19 base pairs

48 (B) TYPE: nucleic acid

49 (C) STRANDEDNESS: single

50 (D) TOPOLOGY: linear

52 (ii) MOLECULE TYPE: DNA (genomic)

57 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

59 ATGCCNGGNA AAGCARATG

19

61 (2) INFORMATION FOR SEQ ID NO: 2:

63 (i) SEQUENCE CHARACTERISTICS:

64 (A) LENGTH: 18 base pairs

65 (B) TYPE: nucleic acid

66 (C) STRANDEDNESS: single

67 (D) TOPOLOGY: linear

69 (ii) MOLECULE TYPE: DNA (genomic)

Errored: Sequence listing must conform to the rules in the CFR as of July 1, 1998.

Must use new format; Contact Robert Wex at

703 306 4119

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/015,078

DATE: 09/10/2001
TIME: 09:39:29

Input Set : A:\235673-1.app
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74 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
76 RAAAYTTCATN GCNCCRTC
78 (2) INFORMATION FOR SEQ ID NO: 3:
80 (i) SEQUENCE CHARACTERISTICS:
81 (A) LENGTH: 135 base pairs
82 (B) TYPE: nucleic acid
83 (C) STRANDEDNESS: single
84 (D) TOPOLOGY: linear
86 (ii) MOLECULE TYPE: DNA (genomic)
91 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
93 ATGCCAGGAA AGCAAATGGC GATTGATGCG GATTAAATT CAGGGCTTAT TGATGATAAG 60
95 GAAGCTAAAA AACGGCGCGC CGCTCTAACG CAAGAAGCGG ATTTTATGG TGCGATGGAT 120
97 GCGCGTCTA AATT 135
99 (2) INFORMATION FOR SEQ ID NO: 4:
101 (i) SEQUENCE CHARACTERISTICS:
102 (A) LENGTH: 28 base pairs
103 (B) TYPE: nucleic acid
104 (C) STRANDEDNESS: single
105 (D) TOPOLOGY: linear
107 (ii) MOLECULE TYPE: DNA (genomic)
112 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
114 CGGGATCCGT GGTTACTAAT GGTTCTAC 28
116 (2) INFORMATION FOR SEQ ID NO: 5:
118 (i) SEQUENCE CHARACTERISTICS:
119 (A) LENGTH: 28 base pairs
120 (B) TYPE: nucleic acid
121 (C) STRANDEDNESS: single
122 (D) TOPOLOGY: linear
124 (ii) MOLECULE TYPE: DNA (genomic)
129 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
131 CGGGATCCTC ATGGCCTCTT CAGAGACC 28
133 (2) INFORMATION FOR SEQ ID NO: 6:
135 (i) SEQUENCE CHARACTERISTICS:
136 (A) LENGTH: 2501 base pairs
137 (B) TYPE: nucleic acid
138 (C) STRANDEDNESS: single
139 (D) TOPOLOGY: linear
141 (ii) MOLECULE TYPE: DNA (genomic)
146 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
148 AGCTTTTTTG TGCCATACTT TTAAACTTTA TATTATAATA AGAGACAAAC ACACCTACCA 60
150 AAATTAAGGC ATTGATTAA GATTATGGCA AACGAACGCT CCAAATTAGC TTTTAAAAAG 120
152 ACTTCCCTG TCTTAAACG CTTCTTGCAA TCCAAAGACT TAGCCCTTGT GGTCTTGTG 180
154 ATAGCGATTT TAGCGATCAT TATCGTGCGC TTACCGCCTT TTGTGTTGGA TTTTTTACTC 240
156 ACGATTTCTA TCGCGCTATC GGTGTTGATT ATTTAATCG GGCTTTATAT TGACAAACCG 300
158 ACTGATTTTA GCGCTTTCCC CACTTTATTA CTCATTGTA CTTTATAACCG CTTGGCTTTA 360
160 AATGTCGCCA CCACTAGAAT GATTTTAACC CAAGGCTATA AAGGGCCTAG CGCGGTGAGC 420
162 ATTATTATCA CGCGCTTGG GGAATTAGC GTGAGCGGGA ATTATGTGAT TGGGGCTATT 480
164 ATCTTTAGTA TTTTAGTGCT GGTGAATTAA TTAGTGGTTA CTAATGGTC TACTAGGGTT 540
166 ACTGAAGTTA GGGCGCGATT TGCCCTAGAC GCTATGCCAG GAAAGCAAAT GGCGATTGAT 600

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/015,078

DATE: 09/10/2001
TIME: 09:39:29

Input Set : A:\235673-1.app
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168 CGGGATTAA ATTCAAGGGCT TATTGATGAT AAGGAAGCTA AAAAACGGCG CGCCGCTCTA 660
 170 AGCCAAGAAG CGGATTTTA TGGTGCATG GATGGCGCGT CTAAATTGAT CAAAGGCGAT 720
 172 GCGATCGCTT CTATCATTAT CACGCTTATC AATATCATTG GGGGTTTTT AGTGGCGTG 780
 174 TTCCAAAGGG ATATGAGCTT GAGCTTAGT GCTAGCACTT TCACTATCTT AACCAATTGGC 840
 176 GATGGGCTTG TAGGGCAAAT CCCTGCCTTA ATCATTGCAGA CACGGACCAGG TATTGTCGCC 900
 178 ACTCGCACCA CGCAAAACGA AGAAGAGGAC TTTGCTTCTA AGCTCATCAC ACAGCTCAC 960
 180 AATAAAAGCA AAACCTTAGT GATTGTGGGG GCGATTATT GCTTTGCAC CATTCCCTGGA 1020
 182 CTCCCTACCT TTTCTTAGC GTTGTAGGG GCTCTCTTT TATTCATCGC ATGGCTGATT 1080
 184 AGCAGGGAGG GAAAGGACGG GTTGCTCACT AAATTAGAAA ATTATTTGAG TCAAAATTC 1140
 186 GGCTTGGATT TGAGCGAAA ACCCCACAGC TCCAAAATCA AACCCACAGC CCCCCACCACA 1200
 188 AGGGCTAAAA CCCAAGAAGA GATTAAAAGA GAAGAAGAGC AAGCCATTGA TGAAGTGTAA 1260
 190 AAAATTGAAT TTTAGAATT GGCTTAGGC TATCAGCTCT ACAGCTTAGC GGACATGAAA 1320
 192 CAAGGGGCG ATTGTTAGA AAGGATTAGG GGTATTAGAA AAAAGATAGC GAGCGATTAT 1380
 194 GGTTTTTGA TGCCCAAAT TAGGATTAGG GATAATTAC AACCCCCCCC AACGCATTAT 1440
 196 GAAATCAAGC TTAAGGGCAT TGTGATTGGT GAAGGCATGG TGATGCCGA TAAGTTTTA 1500
 198 GCCATGAATA CCGGTTTGT GAATAAAAGAA ATTGAAGGCA TTCCTACTAA AGAGCCGGCT 1560
 200 TTTGGAATGG ACGCTTTATG GATTGAAACT AAAAATAAAG AAGAAGCCAT CATTCAGGC 1620
 202 TATACCATTA TTGATCCAAG CACCGTTATT GCGACGCACA CCAGCGAATT AGTAAAAAA 1680
 204 TACGCTGAAG ATTTTATCAC TAAAGATGAA GTGAAATCCC TTTTAGAGCG CTTGGCCAAA 1740
 206 GACTATCCTA CGATTGTAGA AGAGAGTAAA AAAATCCCCA CCGGTGCGAT CCGATCAGTC 1800
 208 TTGCAAGCCT TGTTGCATGA AAAAATCCCC ATTAAAGACA TGCTCACTAT TTTAGAAACG 1860
 210 ATTACCGATA TTGCGCCATT AGTCAAAAC GATGTGAATA TCTTAACCGA ACAAGTGAGG 1920
 212 GCGAGGCTT CTAGGGTGAT CACTAACGCT TTTAAATCTG AAGACGGCG TTTGAAATT 1980
 214 TTAACCTTT CTACCGATAG CGAACAAATT TTGCTTAATA AATTGCGAGA AAATGGCACT 2040
 216 TCTAAGAGCC TACTACTCAA TGTGGGCCAA TTGCAAAAC TCATTGAAGC GGTCTCTGAA 2100
 218 GAGGCCATGA AAGTCTTGCA AAAAGGGATC GCTCCGGTGA TTTTGATCGT AGAGCCTAAT 2160
 220 TTAAGAAAAG CCCTTTCTAA TCAAATGGAG CAGGCTAGGA TTGATGTAAT CGTGTAAAGC 2220
 222 CATGCTGAAT TAGATCCTAA CTCTAATTG GAAGCCTTAG GCACGATCCA TATTAACCTT 2280
 224 TAAGGGATAA ATAATTGATA AAAAAGGAGA ATGATGCAAG TTTATCACCT TTCACACATT 2340
 226 GATTAGACG GCTATGCATG CCAGCTTGT TCAAAACAAT TTTTTAAAAA TATCCAATGC 2400
 228 TATAACGCTA ATTACGGCG TGAAGTCTCA GCGAGAATTG ATGAGATTG AAACCGGATC 2460
 230 GCTCAATCTA AAGAGAGTGA ATTCCATTATT TTGATTAGCG A 2501
 232 (2) INFORMATION FOR SEQ ID NO: 7:
 234 (i) SEQUENCE CHARACTERISTICS:
 235 (A) LENGTH: 732 amino acids
 236 (B) TYPE: amino acid
 237 (C) STRANDEDNESS: single
 238 (D) TOPOLOGY: linear
 240 (ii) MOLECULE TYPE: peptide
 245 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
 247 Met Ala Asn Glu Arg Ser Lys Leu Ala Phe Lys Lys Thr Phe Pro Val
 248 1 5 10 15
 250 Phe Lys Arg Phe Leu Gln Ser Lys Asp Leu Ala Leu Val Val Phe Val
 251 20 25 30
 253 Ile Ala Ile Leu Ala Ile Ile Val Pro Leu Pro Pro Phe Val Leu
 254 35 40 45
 256 Asp Phe Leu Leu Thr Ile Ser Ile Ala Leu Ser Val Leu Ile Ile Leu
 257 50 55 60
 259 Ile Gly Leu Tyr Ile Asp Lys Pro Thr Asp Phe Ser Ala Phe Pro Thr

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/015,078

DATE: 09/10/2001

TIME: 09:39:29

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260	65	70	75	80												
262	Leu	Leu	Leu	Ile	Val	Thr	Leu	Tyr	Arg	Leu	Ala	Leu	Asn	Val	Ala	Thr
263																
265		85							90							95
266	Thr	Arg	Met	Ile	Leu	Thr	Gln	Gly	Tyr	Lys	Gly	Pro	Ser	Ala	Val	Ser
268																
269		100							105							110
271	Ile	Ile	Ile	Thr	Ala	Phe	Gly	Glu	Phe	Ser	Val	Ser	Gly	Asn	Tyr	Val
272																
274		115							120							125
275	Ile	Gly	Ala	Ile	Ile	Phe	Ser	Ile	Leu	Val	Leu	Val	Asn	Leu	Leu	Val
277																
278		130							135							140
280	Val	Thr	Asn	Gly	Ser	Thr	Arg	Val	Thr	Glu	Val	Arg	Ala	Arg	Phe	Ala
281																
283	145		150							155						160
284	Leu	Asp	Ala	Met	Pro	Gly	Lys	Gln	Met	Ala	Ile	Asp	Ala	Asp	Leu	Asn
286																
288	165									170						175
289	Ser	Gly	Leu	Ile	Asp	Asp	Lys	Glu	Ala	Lys	Lys	Arg	Arg	Ala	Ala	Leu
290																
292	180								185							190
293	Ser	Gln	Glu	Ala	Asp	Phe	Tyr	Gly	Ala	Met	Asp	Gly	Ala	Ser	Lys	Phe
294																
295	195								200							205
296	Val	Lys	Gly	Asp	Ala	Ile	Ala	Ser	Ile	Ile	Ile	Thr	Leu	Ile	Asn	Ile
297										215						220
298	Ile	Gly	Gly	Phe	Leu	Val	Gly	Val	Phe	Gln	Arg	Asp	Met	Ser	Leu	Ser
299										230						240
301	Phe	Ser	Ala	Ser	Thr	Phe	Thr	Ile	Leu	Thr	Ile	Gly	Ala	Gly	Leu	Val
302											245					255
304	Gly	Gln	Ile	Pro	Ala	Leu	Ile	Ile	Ala	Thr	Arg	Thr	Gly	Ile	Val	Ala
305											260					270
307	Thr	Arg	Thr	Thr	Gln	Asn	Glu	Glu	Glu	Asp	Phe	Ala	Ser	Lys	Leu	Ile
308										275						285
310	Thr	Gln	Leu	Thr	Asn	Lys	Ser	Lys	Thr	Leu	Val	Ile	Val	Gly	Ala	Ile
311										290						300
313	Tyr	Cys	Phe	Cys	Thr	Ile	Pro	Gly	Leu	Pro	Thr	Phe	Ser	Leu	Ala	Phe
314										310						320
316	Val	Gly	Ala	Leu	Phe	Leu	Phe	Ile	Ala	Trp	Leu	Ile	Ser	Arg	Glu	Gly
317										325						335
319	Lys	Asp	Gly	Leu	Leu	Thr	Lys	Leu	Glu	Asn	Tyr	Leu	Ser	Gln	Lys	Phe
320										340						350
322	Glu	Gln	Ala	Ile	Asp	Glu	Val	Leu	Lys	Ile	Glu	Phe	Leu	Glu	Leu	Ala
323										355						365
325	Leu	Gly	Thr	Gln	Leu	Tyr	Ser	Leu	Ala	Asp	Met	Lys	Gln	Gly	Gly	Asp
326										370						380
328	Leu	Leu	Glu	Arg	Ile	Arg	Gly	Ile	Arg	Lys	Lys	Ile	Ala	Ser	Asp	Tyr
329										390						400
331	Gly	Phe	Leu	Met	Pro	Gln	Ile	Arg	Ile	Arg	Asp	Asn	Leu	Gln	Leu	Pro
332										405						415
	435									420						430
	450									440						445
										455						460

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PATENT APPLICATION: US/09/015,078

DATE: 09/10/2001
TIME: 09:39:29

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334 Met Val Met Pro Asp Lys Phe Leu Ala Met Asn Thr Gly Phe Val Asn
 335 465 470 475 480
 337 Lys Glu Ile Glu Gly Ile Pro Thr Lys Glu Pro Ala Phe Gly Met Asp
 338 485 490 495
 340 Ala Leu Trp Ile Glu Thr Lys Asn Lys Glu Glu Ala Ile Ile Gln Gly
 341 500 505 510
 343 Tyr Thr Ile Ile Asp Pro Ser Thr Val Ile Ala Thr His Thr Ser Glu
 344 515 520 525
 346 Leu Val Lys Lys Tyr Ala Glu Asp Phe Ile Thr Lys Asp Glu Val Lys
 347 530 535 540
 349 Ser Leu Leu Glu Arg Leu Ala Lys Asp Tyr Pro Thr Ile Val Glu Glu
 350 545 550 555 560
 352 Ser Lys Lys Ile Pro Thr Gly Ala Ile Arg Ser Val Leu Gln Ala Leu
 353 565 570 575
 355 Leu His Glu Lys Ile Pro Ile Lys Asp Met Leu Thr Ile Leu Glu Thr
 356 580 585 590
 358 Ile Thr Asp Ile Ala Pro Leu Val Gln Asn Asp Val Asn Ile Leu Thr
 359 595 600 605
 361 Glu Gln Val Arg Ala Arg Leu Ser Arg Val Ile Thr Asn Ala Phe Lys
 362 610 615 620
 364 Ser Glu Asp Gly Arg Leu Lys Phe Leu Thr Phe Ser Thr Asp Ser Glu
 365 625 630 635 640
 367 Gln Phe Leu Leu Asn Lys Leu Arg Glu Asn Gly Thr Ser Lys Ser Leu
 368 645 650 655
 370 Leu Leu Asn Val Gly Glu Leu Gln Lys Leu Ile Glu Ala Val Ser Glu
 371 660 665 670
 373 Glu Ala Met Lys Val Leu Gln Lys Gly Ile Ala Pro Val Ile Leu Ile
 374 675 680 685
 376 Val Glu Pro Asn Leu Arg Lys Ala Leu Ser Asn Gln Met Glu Gln Ala
 377 690 695 700
 379 Arg Ile Asp Val Ile Val Leu Ser His Ala Glu Leu Asp Pro Asn Ser
 380 705 710 715 720
 382 Asn Phe Glu Ala Leu Gly Thr Ile His Ile Asn Phe
 383 725 730

385 (2) INFORMATION FOR SEQ ID NO: 8:

387 (i) SEQUENCE CHARACTERISTICS:
 388 (A) LENGTH: 732 amino acids
 389 (B) TYPE: amino acid
 390 (C) STRANDEDNESS: single
 391 (D) TOPOLOGY: linear

393 (ii) MOLECULE TYPE: peptide

398 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

400 Met Ala Asn Glu Arg Ser Lys Leu Ala Phe Lys Lys Thr Phe Pro Val
 401 1 5 10 15
 403 Phe Lys Arg Phe Leu Gln Ser Lys Asp Leu Ala Leu Val Val Phe Val
 404 20 25 30
 406 Ile Ala Ile Leu Ala Ile Ile Ile Val Pro Leu Pro Pro Phe Val Leu
 407 35 40 45
 409 Asp Phe Leu Leu Thr Ile Ser Ile Ala Leu Ser Val Leu Ile Ile Leu

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/015,078

DATE: 09/10/2001

TIME: 09:39:30

Input Set : A:\235673-1.app

Output Set: N:\CRF3\09102001\I015078.raw

L:30 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:31 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]